

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2003, 22:06:02 ; Search time 2719.38 Seconds

(without alignments)
12110.308 Million cell updates/sec

Title: us-09-904-568-3

Perfect score: 1355
Sequence: 1 gggcagcagcgttgagtgga.....gtgttcagcagcagcccg 1355

Scoring table:

IDENTITY_MUC
Gapop 10.0 , Gapept 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 6312

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hnc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hum:*
19: em_gss_pln:*
20: em_gss_vtc:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	1.0	19	A1702520	A1702520 tz67g05.x
2	14	1.0	28	A2345513	A2345513 1M0080J04
3	13.6	1.0	20	A2764505	A2764505 1M0560M06
4	13.4	1.0	19	AA928040	AA928040 o158g09.s

5	13.4	1.0	19	28	A2465954	A2465954 1M0276E16
6	13.4	1.0	19	28	A2466389	A2466389 1M0314E21
7	13.4	1.0	20	9	AL587572	AL587572 AL587572
8	13.4	1.0	20	28	A2821905	A2821905 2M0094D20
9	13.2	1.0	19	28	A2429998	A2429998 1M0214F16
10	13.2	1.0	19	28	A2456215	A2456215 1M0258K21
11	13	1.0	18	12	BM658677	BM658677 LZV602768
12	13	1.0	19	28	A2360314	A2360314 1M0103G03
13	13	1.0	19	28	A2513919	A2513919 1M0360E13
14	13	1.0	19	28	A2645841	A2645841 1M0511G04
15	12.8	0.9	18	9	AL048754	AL048754 DKF5P566L
16	12.8	0.9	19	28	A2819620	A2819620 2M0091A23
17	12.8	0.9	19	28	A2995149	A2995149 2M0280D22
18	12.8	0.9	20	2	HSW002936	AL038460 Homo sapi
19	12.8	0.9	20	28	A2430735	A2430735 1M0215A22
20	12.8	0.9	20	28	A2468517	A2468517 1M0281N01
21	12.8	0.9	20	28	A2628029	A2628029 1M0476F17
22	12.8	0.9	20	28	A2665192	A2665192 1M0546C04
23	12.8	0.9	20	29	TA339H11Q	AL492631 T. brucei
24	12.6	0.9	19	9	AL584018	AL584018 ts12e10.x
25	12.6	0.9	19	28	A2394490	A2394490 1M0158O05
26	12.6	0.9	19	28	A2422163	A2422163 1M0200B22
27	12.6	0.9	19	28	A2427411	A2427411 1M0209A22
28	12.6	0.9	19	28	A2759607	A2759607 1M0552123
29	12.6	0.9	19	28	A2775624	A2775624 2M008E01
30	12.6	0.9	19	28	A2825396	A2825396 2M0100N04
31	12.6	0.9	20	14	C20903	C20903 HUM65000498
32	12.6	0.9	20	28	A2386659	A2386659 1M0145G15
33	12.6	0.9	20	28	A2426873	A2426873 1M0208L05
34	12.6	0.9	20	28	A2469472	A2469472 1M0283A06
35	12.6	0.9	20	28	A2466787	A2466787 1M0315D23
36	12.6	0.9	20	28	A2633741	A2633741 1M0489G12
37	12.6	0.9	20	28	A2823352	A2823352 2M0097A22
38	12.6	0.9	20	28	A2830285	A2830285 2M0109N22
39	12.4	0.9	16	13	B0590207	B0590207 E012843-0
40	12.4	0.9	19	28	A2308423	A2308423 1M0011E21
41	12.4	0.9	19	28	A2474038	A2474038 1M0290G15
42	12.4	0.9	19	28	A2585820	A2585820 1M0391I15
43	12.4	0.9	19	28	A2650252	A2650252 1M0520N17
44	12.4	0.9	20	9	AL587727	AL587727 AL587727
45	12.4	0.9	20	28	A2345856	A2345856 1M0080G17

ALIGNMENTS

RESULT 1
A1702520/c 19 bp mRNA linear EST 16-DEC-1999
LOCUS tz67g05.x1 NCI-CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2293688 3'
DEFINITION similar to WP:DI007.7 CE09042 RNA-BINDING PROTEIN ; contains element
MSRL Repetitive element ;, mRNA sequence.

ACCESSION A1702520
VERSION A1702520.1 GI:4990420
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL COMMENT

Unpublished
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMIL at:
www-bio.llnl.gov/bdrp/image/image.html

Trace considered overall poor quality

Insert length: 2437 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2293688"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: PCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

BASE COUNT
2 a 2 c 15 g 0 t

ORIGIN

Query Match 1.0%; Score 14.2; DB 9; Length 19;
Best Local Similarity 84.2%; Pred. No. 5e+07;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 184 TTCCCGCGCGCCACCGG 202
19 TTCCCGCGCGCGCCCGG 1
|||||

RESULT 2
A2345513 20 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0080J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0080J04 F, genomic survey sequence.
ACCESSION A2345513
VERSION A2345513.1 GI:10424750
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0080 row: J column: 04
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080J04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

FEATURES
Source

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel.
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (ql1473211419b1AF139072.1), a copy number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance.

BASE COUNT
3 a 13 c 0 g 4 t

ORIGIN

Query Match 1.0%; Score 14; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.7e+07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1208 ACCCTCCCTCCCT 1221
Db 1 ACCCTCCCTCCCT 14
|||||

RESULT 3
A2764505 20 bp DNA linear GSS 16-FEB-2001
LOCUS 1M0560M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0560M06 R, genomic survey sequence.
ACCESSION A2764505
VERSION A2764505.1 GI:12879537
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0560 row: M column: 06
Seq primer: CACACGAGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560M06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

FEATURES
Source

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 0 a 15 c 5 g 0 t

Query Match 1.0%; Score 13.6; DB 28; Length 20;
Best Local Similarity 80.0%; Pred. No. 7e+07;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 186 CCCCCCGCCCGCCGACG 205
11111111111111111111
1 CCCCCCGCCCGCCGCGGCG 20

RESULT 4 19 bp mRNA linear EST 22-APR-1998
AA928040 0158609.s1 NCI CGAP_HN4 Homo sapiens CDNA clone IMAGE:1486912 3'
LOCUS similar to TR:004216 004216 EXTENSTN: contains element MSRI
DEFINITION repetitive element; mRNA sequence.

ACCESSION AA928040 GI:3077196
VERSION AA928040.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 19)
AUTHORS NCI/NIH-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-f@mail.nih.gov
Tissue Procurement: John Ensley, M.D.
CDNA Library Preparation: Stratagene, Inc.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.lnl.gov/bdrp/image/image.html

FEATURES
source Trace considered overall poor quality
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..19

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1486912"
/tissue_type="squamous cell carcinoma"
/lab_host="SOLR (kanamycin resistant)"
/clone_1lb="NCI_CGAP_HN4"
/note="Organ: pharynx; Vector: Bluescript SK-; Site: 1;
ECORI: Site: 2; XhoI: Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.5 kb. 5' adaptor sequence:

5' GAATTCGCGACGAG 3' 3' adaptor sequence: 5' (GA
1)ACATGCTCGAGTCTTTTCTTTTCTTTT 3'."

BASE COUNT 2 a 1 c 11 g 5 t

Query Match 1.0%; Score 13.4; DB 9; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.7e+07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 659 TGGTGGGAGCTGG 673
11111111111111111111
5 TGGTGGGAGCTGG 19

RESULT 5 19 bp DNA linear GSS 04-OCT-2000
AZ465954 1M0276E16F Mouse 10kb plasmid U0GCM1 library Mus musculus genomic
LOCUS clone U0GCM10276E16 F, genomic survey sequence.
DEFINITION

ACCESSION AZ465954 GI:10624079
VERSION AZ465954.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0276 row: E column: 16
Seq primer: CGTGTGAACGACGCCACCT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U0GCM10276E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid U0GCM1 library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g114732114[9b]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
0 a 5 c 0 g 14 t

Query Match
Best Local Similarity 93.3%; Pred. No. 7.7e+07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1142 CCTTTTCTTTT 1156
|||||
DB 4 CCTTTTCTTTT 18

RESULT 6
LOCUS A2486389/c
DEFINITION 19 bp DNA linear GSS 05-OCT-2000
clone U06C1M0314E21 F, genomic survey sequence.

ACCESSION A2486389
VERSION A2486389.1 GI:10653117
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah
Bldg. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0314 row: E column: 21
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0314E21"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
7 a 2 c 7 g 3 t

Query Match
Best Local Similarity 93.3%; Pred. No. 7.7e+07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1062 CCTTCCATCAGGCA 1076
|||||
DB 18 CCTTCCATCAGGCA 4

RESULT 7
LOCUS AL587572
DEFINITION 20 bp mRNA linear EST 02-MAR-2001
ROS059B11, mRNA sequence.

ACCESSION AL587572
VERSION AL587572.1 GI:13192606
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
AUTHORS 1 (bases 1 to 20)
Murray, F.
BP Chicken Brain Library
Unpublished
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (*6854-1)
Seq primer: M13F.
Location/Qualifiers
1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059B11"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; site1: NotI; site2: SalI; cloned unidirectionally; Primer: Oligo dt, 5' adaptor sequence: 5'-TCGACCTCGAG 3', 3' adaptor sequence: 5'-GCGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (*6854-1)"

TITLE BP Chicken Brain Library
JOURNAL Unpublished
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (*6854-1)
Seq primer: M13F.
Location/Qualifiers
1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059B11"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; site1: NotI; site2: SalI; cloned unidirectionally; Primer: Oligo dt, 5' adaptor sequence: 5'-TCGACCTCGAG 3', 3' adaptor sequence: 5'-GCGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (*6854-1)"

FEATURES
source
1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059B11"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; site1: NotI; site2: SalI; cloned unidirectionally; Primer: Oligo dt, 5' adaptor sequence: 5'-TCGACCTCGAG 3', 3' adaptor sequence: 5'-GCGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (*6854-1)"

BASE COUNT
ORIGIN
0 a 0 c 2 g 18 t

Query Match
Best Local Similarity 93.3%; Pred. No. 7.8e+07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1144 TTTTCTTTTGG 1158
|||||
DB 6 TTTTCTTTTGG 20

RESULT 8
LOCUS A2821905/c
DEFINITION 20 bp DNA linear GSS 20-FEB-2001
A2821905

DEFINITION 2M0094D20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0094D20 R, genomic survey sequence.

ACCESSION A2821905

VERSION A2821905.1 GI:12991813

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 20
Seq primer: CACACAGAAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

1..20
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0094D20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (g1473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 18 a 2 c 0 g 0 t

ORIGIN

Query Match 1.0%; Score 13.4; DB 28; Length 20;
Best Local Similarity 93.3%; Pred. No. 7.8e+07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1144 TTTTTCCTTTTGG 1158
||||| |||||||
Db 15 TTTTTCCTTTTGG 1

RESULT 9
A2429998/c

LOCUS A2429998 19 bp DNA linear GSS 03-OCT-2000

DEFINITION IM0214F16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0214F16 F, genomic survey sequence.

ACCESSION A2429998

VERSION A2429998.1 GI:10554011

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0214 row: F column: 16
Seq primer: CGTTGTAAACGACGGCCACT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1..19
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0214F16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (g1473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 3 c 9 g 2 t

ORIGIN

Query Match 1.0%; Score 13.2; DB 28; Length 19;
Best Local Similarity 83.3%; Pred. No. 8.6e+07;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 631 CTCACGAGCTCTGCATC 648
||||| |||||||
Db 18 CTCACGAGCTCTGCATC 1

RESULT 10

University of Utah Genome Center
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0258 row: k column: 21
Seq primer: CACACAGCAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

Location/Qualifiers
1. .19

4	a	3	c	3	g	9	e
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Query Match	1.0%;	Score 13.2;	DB 28;	Length 19;
Best Local Similarity	83.3%;	Pred. No. 8.6e+07;		
Matches 15;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	1173	AAACATGTTTCTATAGT	1190
Db	2	ACACCTGTTTATAGT	19

RESULT	11
BM658677	
LOCUS	
DEFINITION	BM658677 18 bp mRNA linear EST 27-FEB-2002
ACCESSION	LZ7602768363.R1 CSECFXJ37 pig adrenal Sus scrofa cDNA, mRNA sequence.
VERSION	BM658677
KEYWORDS	BM658677.1 GI:18958948
SOURCE	EST.
ORGANISM	Sus scrofa (pig)
	Sus scrofa

REFERENCE	1 (bases 1 to 18)
AUTHORS	Adelson, D.L. and Gill, C.A.
TITLE	Porcine ESTs
JOURNAL	Unpublished
COMMENT	Contact: David L. Adelson

Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471
USA
Tel: 97988452616
Fax: 97988456970
Email: david.edelison@tamu.edu.
Location/Qualifiers

FEATURES
source

87.1

```

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone_lib="CSBQFXL37 pig adrenal"
/note="Organ: adrenal gland; Vector: pBluescript SK+;
Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNinsert)
GGGATTTGGAGCTCCACCGGCGGGGGCGGCGGCTTCGAG. Sequence 3' c
the inserts (AAGATTCGATATCAACATTCATGATACCTGACCTCGAG.
non-normalized library, sequenced 3' with M13R primer."
BASE COUNT
0 a 1 c 0 g 17 t

```

BASE COUNT
ORIGIN

Query Match	1.0%;	Score 13;	DB 12;	Length 18;
Best Local Similarity	100.0%;	Pred. NO. 9.5e+07;		
Matches 13; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1144	TTTTTCTTTT	1156
		TTTTTTTTTT	
Db	2	TTTTTCTTTT	14

RESULT 12	LOCUS	DEFINITION	ACCSSION	VERSION	KEYWORDS	SOURCE
A2360314/c						
A2360314	19 bp	DNA	1linear	GSS	02-OCT-2000	
1M0103063R	mouse	10kb	plasmid	UUGC1M	library	Mus musculus genomic
clone UUGC1M0103063 R,						genomic survey sequence.
A2360314						
A2360314.1	GI:10474014					
GSS.						
Mus musculus (house mouse)						

REFERENCE
AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT

Contact: Robert B. Weiss
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Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0103 row: G column: 03
 Seq primer: CACACAGAAACGACGATACCC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

1. 19
 Location/Qualifiers

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U08C1M0103G03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid U08C1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gplAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 17 a 0 c 2 g 0 t
 ORIGIN

Query Match 1.0%; Score 13; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.6e+07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 TTTTTCCTTTT 1156
 |||||||
 DB 16 TTTTTCCTTTT 4

RESULT 13
 AZ513919 19 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0360E13F Mouse 10kb plasmid U08C1M library Mus musculus genomic
 DEFINITION clone U08C1M0360E13 F, genomic survey sequence.
 ACCESSION AZ513919
 VERSION AZ513919.1 GI:10695235
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0360 row: E column: 13
 Seq primer: CGTTGTAAACGACGCGCATG
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

1. 19
 Location/Qualifiers

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U08C1M0360E13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid U08C1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gplAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 1 c 0 g 18 t
 ORIGIN

Query Match 1.0%; Score 13; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.6e+07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 TTTTTCCTTTT 1156
 |||||||
 DB 5 TTTTTCCTTTT 17

RESULT 14
 AZ645841 19 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0511G04R Mouse 10kb plasmid U08C1M library Mus musculus genomic
 DEFINITION clone U08C1M0511G04 R, genomic survey sequence.
 ACCESSION AZ645841
 VERSION AZ645841.1 GI:11775726
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0511 row: 6 column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1.19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0511G04"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
18 t
1 c 0 g

BASE COUNT

0 a
1 c
18 t

ORIGIN

Query Match 1.0%; Score 13; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.6e+07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1144 TTTTTCCTTTT 1156
|||||
2 TTTTTCCTTTT 14

Db

RESULT 15

AL048754 18 bp mRNA linear EST 30-APR-1999

LOCUS AL048754/c
DEFINITION DKFZP566L173-r1 566 (synonym: hfxd2) Homo sapiens cDNA clone

ACCESSION AL048754
VERSION DKFZP566L173, mRNA sequence.

KEYWORDS AL048754.1 GI:4727825

SOURCE EST.
Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 18)
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

TITLE EST (Koehler, et al.)

JOURNAL Unpublished

COMMENT Contact: Koehler K

FEATURES
source
1.18
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566L173"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfxd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
16 a
1 c 0 g
1 t

BASE COUNT

16 a
1 c
1 t

ORIGIN

Query Match 0.9%; Score 12.8; DB 9; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.1e+08;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1144 TTTTTCCTTTTGA 1159
|||||
16 TTTTTCCTTTTGA 1

Db

Search completed: September 8, 2003, 02:28:52
Job time: 2723.38 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2003, 18:52:18 ; Search time 362.069 Seconds

(without alignments)
8607.385 Million cell updates/sec

Title: US-09-904-568-3

Perfect score: 1335

Sequence: 1 gggcagcgagttgagtgga.....gtgttcagcgagggcccg 1355

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1537136 seqs, 1149988732 residues 277732

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCT05_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	1.2	18	11	US-09-876-235-29
2	16	1.2	17	12	US-09-792-818-388
3	15.8	1.2	17	12	US-09-792-818-389
4	15.8	1.2	20	10	US-09-791-243-25
5	15.8	1.2	20	11	US-09-842-758-79
6	15.8	1.2	20	12	US-10-006-972A-87
7	15.4	1.1	18	9	US-10-005-715-2
8	15.4	1.1	18	9	US-09-813-289-4
9	15.4	1.1	18	12	US-09-809-280-19
10	15.4	1.1	20	12	US-10-024-360-81
11	15.2	1.1	20	10	US-09-780-172-69
12	15.2	1.1	20	11	US-09-989-420-23
13	15.2	1.1	20	11	US-09-948-002-55
14	15.2	1.1	20	11	US-09-954-556-94
15	15.2	1.1	20	14	US-10-116-949-33
16	15.2	1.1	20	14	US-10-116-949-43

17	15.2	1.1	20	14	US-10-067-443-16	Sequence 16, Appl
18	15.2	1.1	20	14	US-10-271-887-168	Sequence 168, App
19	15	1.1	17	12	US-09-792-818-387	Sequence 387, App
20	15	1.1	17	12	US-09-792-818-390	Sequence 390, App
21	14.8	1.1	19	10	US-09-969-373-1795	Sequence 1795, Ap
22	14.8	1.1	20	11	US-09-539-382-23	Sequence 23, Appl
23	14.8	1.1	20	11	US-09-919-197-42	Sequence 42, Appl
24	14.8	1.1	20	14	US-10-067-790-23	Sequence 23, Appl
25	14.8	1.1	20	14	US-10-067-692-23	Sequence 23, Appl
26	14.8	1.1	20	14	US-10-067-693-23	Sequence 23, Appl
27	14.8	1.1	20	14	US-10-263-872-35	Sequence 35, Appl
28	14.4	1.1	17	10	US-09-864-785-1485	Sequence 1485, Ap
29	14.4	1.1	17	10	US-09-864-785-2738	Sequence 2738, Ap
30	14.4	1.1	18	10	US-09-880-732-49	Sequence 49, Appl
31	14.4	1.1	18	11	US-09-967-237-113	Sequence 113, App
32	14.4	1.1	19	10	US-09-880-732-50	Sequence 50, Appl
33	14.4	1.1	20	8	US-08-983-605-364	Sequence 364, App
34	14.4	1.1	20	9	US-09-752-983-48	Sequence 48, Appl
35	14.4	1.1	20	10	US-09-877-935-7	Sequence 7, Appl
36	14.4	1.1	20	11	US-09-863-049A-17	Sequence 17, Appl
37	14.4	1.1	20	11	US-09-920-033-109	Sequence 109, App
38	14.2	1.0	19	11	US-09-880-313A-120	Sequence 120, App
39	14.2	1.0	20	9	US-09-758-881-68	Sequence 16, Appl
40	14.2	1.0	20	9	US-09-992-901-4	Sequence 68, Appl
41	14.2	1.0	20	9	US-09-774-809-123	Sequence 123, App
42	14.2	1.0	20	11	US-09-915-485-52	Sequence 52, Appl
43	14.2	1.0	20	11	US-09-953-047-85	Sequence 85, Appl
44	14.2	1.0	20	11	US-09-972-607-44	Sequence 44, Appl
45	14.2	1.0	20	11		

ALIGNMENTS

RESULT 1
US-09-876-235-29
Sequence 29, Application US/09876235
Publication No. US2003002236A1
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rife
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350005
CURRENT APPLICATION NUMBER: US/09/876, 235
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005
PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-876-235-29
Query Match 1.28; Score 16.4; DB 11; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 679 GTGTTATTTGGAGCCAG 696
Db 1 GTGTTATTTGGAGCCAG 18

RESULT 2

US-09-792-818-388/c
; Sequence 388, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: MCSwigen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 388
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-388

Query Match 1.2%; Score 16; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 299 CTGCTGTGGGGCTGC 314
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Db 17 CTGCTGTGGGGCTGC 2

RESULT 3
US-09-792-818-389/c
; Sequence 389, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: MCSwigen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 389
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-389

Query Match 1.2%; Score 16; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 299 CTGCTGTGGGGCTGC 314
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Db 16 CTGCTGTGGGGCTGC 1

RESULT 4
US-09-791-243-25/c
; Sequence 25, Application US/09791243
; Patent No. US20020147164A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Robert Rothlein
; APPLICANT: Takashi Kei Kishimoto

APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOHESTEIN-1 EXPRESSION
; FILE REFERENCE: RTS-0095
; CURRENT APPLICATION NUMBER: US/09/791,243
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-791-243-25

Query Match 1.2%; Score 15.8; DB 10; Length 20;
Best Local Similarity 89.5%; Pred. No. 5.1e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 521 ACCTCCGAGAGAGCT 539
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Db 20 ACCTCCGAGAGAGCTCT 2

RESULT 5
US-09-842-758-79/c
; Sequence 79, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Verneil, Corine A. M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkets, Richard A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kund
; APPLICANT: Tcherenev, Velizar T
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E
; APPLICANT: Gangoli, Esna A
; APPLICANT: Smithson, Glennda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Grose, William M
; APPLICANT: Edward, Szekeres S
; APPLICANT: Alsobrook II, John P
; TITLE OF INVENTION: No. US20030083244A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,158
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,007
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,236
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,238
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,186
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,474
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/201,508
; PRIOR FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/265,160
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 79
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Ag743 Forward
US-09-842-758-79

Query Match 1.2%; Score 15.8; DB 11; Length 20;
Best Local Similarity 89.5%; Pred. No. 5.1e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 641 TCCTGATCCCCCAAGACT 659
DB 19 TCCTGATCCACCAAGACT 1

RESULT 6
US-10-006-972A-87/C
Sequence 87, Application US/10006972A
Publication No. US20030139359A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 3 EXPRESSION
FILE REFERENCE: PFS-0335
CURRENT APPLICATION NUMBER: US/10/006,972A
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 87
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-972A-87

Query Match 1.2%; Score 15.8; DB 12; Length 20;
Best Local Similarity 89.5%; Pred. No. 5.1e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 631 CTCGAGAGCTGTGATCC 649
DB 19 CTCGAGAGTTCCTCATCC 1

RESULT 7
US-10-005-715-2/C
Sequence 2, Application US/10005715
Publication No. US20030023058A1
GENERAL INFORMATION:
APPLICANT: University of No. US20030023058A1th Carolina at Chapel Hill
APPLICANT: Weston, Brent W.
APPLICANT: Hillier, Kara M.
TITLE OF INVENTION: ANTISENSE HUMAN FUCOSYLTRANSFERASE SEQUENCES AND METHODS OF USE
FILE REFERENCE: 5470-259CT
CURRENT APPLICATION NUMBER: US/10/005,715
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/131,068
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentln version 3.1
SEQ ID NO 2

LENGTH: 20
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-10-005-715-2

Query Match 1.2%; Score 15.8; DB 14; Length 20;
Best Local Similarity 89.5%; Pred. No. 5.1e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1322 CTTTGTAGATCTTGCTT 1340
DB 19 CTTTGTAGATCTTCACTT 1

RESULT 8
US-09-813-289-4/C
Sequence 4, Application US/09813289
Patent No. US20020061571A1
GENERAL INFORMATION:
APPLICANT: Mahadevan, M.S.
APPLICANT: Tiscornia, G.
TITLE OF INVENTION: No. US20020061571A1el isoform of myotonic dystrophy associated
FILE REFERENCE: 800.027US1
CURRENT APPLICATION NUMBER: US/09/813,289
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,590
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-813-289-4

Query Match 1.1%; Score 15.4; DB 9; Length 18;
Best Local Similarity 94.1%; Pred. No. 6.4e+05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 578 AGGCCCTCGCTGCCCC 594
DB 17 AGGCCCTCGACTGCCCC 1

RESULT 9
US-09-809-920-19/C
Sequence 19, Application US/09809920
Publication No. US20030139584A1
GENERAL INFORMATION:
APPLICANT: Satc, Takaaki
TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING
THEREOF
EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/809,920
FILING DATE: 16-Mar-2001
CLASSIFICATION: <Unknown>

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/156,191
; FILING DATE: <UNKNOWN>
; ATTORNEY/AGENT INFORMATION:
;   NAME: White, John P.
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 0575/51902
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 278-0400
;   TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 18 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-809-920-19

Query Match
Best Local Similarity 1.1%; Score 15.4; DB 12; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 627 CCAGCTCCAGCAGCTCT 643
Db 18 CCAGCTGCAGCAGCTCT 2

RESULT 10
US-10-024-369-81/c
; Sequence 81, Application US/10024369
; Publication No. US20030134809a1
; GENERAL INFORMATION:
;   APPLICANT: Alexander H. Borchers
;   APPLICANT: Donna T. Ward
;   APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF ABC TRANSPORTER MHC 1 EXPRESSION
; FILE REFERENCE: RFS-0353
; CURRENT APPLICATION NUMBER: US/10/024,369
; CURRENT FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 81
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-369-81

Query Match
Best Local Similarity 1.1%; Score 15.4; DB 12; Length 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 785 CCACCAGCGCCCTGGCT 801
Db 17 CCACCAGTGCCTGGAT 1

RESULT 11
US-09-780-172-69/c
; Sequence 69, Application US/09780172
; Patent No. US20020147163a1
; GENERAL INFORMATION:
;   APPLICANT: Robert McKay
;   APPLICANT: Susan M. Freiler
;   APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
; FILE REFERENCE: RFS-0159
; CURRENT APPLICATION NUMBER: US/09/780,172
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 69
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-172-69

Query Match
Best Local Similarity 1.1%; Score 15.2; DB 10; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1070 TCAGGACGCTCTCAGTGA 1089
Db 20 TCTGCGACGCTCACCAGTGA 1

RESULT 12
US-09-989-420-23/c
; Sequence 23, Application US/09989420
; Publication No. US20030013671a1
; GENERAL INFORMATION:
;   APPLICANT: MINENO, Junichi et al.
; TITLE OF INVENTION: Genomic DNA library
; FILE REFERENCE: 1422-0506P
; CURRENT APPLICATION NUMBER: US/09/989,420
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: a sequence of a primer for
US-09-989-420-23

Query Match
Best Local Similarity 1.1%; Score 15.2; DB 11; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1238 TCGTGGAGCTGGCCATGTGA 1257
Db 20 TCGGCGAGCTGACATCTGA 1

RESULT 13
US-09-948-002-55
; Sequence 55, Application US/09948002
; Publication No. US20030050265a1
; GENERAL INFORMATION:
;   APPLICANT: Nicholas M. Dean
;   APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-55

Query Match
Best Local Similarity 1.1%; Score 15.2; DB 11; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 621 CAGGAGCAGCTCCAGAGC 640
1 |||||
Db 1 CCGGAGCAGATGACAGAGC 20

Db 1 CTGGTGATGTCACAGAGC 20
Search completed: September 7, 2003, 22:23:28
Job time: 363.069 secs

RESULT 14

US-09-954-556-94
; Sequence 94, Application US/09954556
; Publication No. US20030078219A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freiler
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 94
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-954-556-94

Query Match

Best Local Similarity 1.1%; Score 15.2; DB 11; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.8e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY

856 TACCGCTTGAGGTCCCCAC 875
1 |||||
Db 1 TGCCTCTGTGAGGTCCCCAC 20

RESULT 15

US-10-116-949-33
; Sequence 33, Application US/10116949
; Publication No. US20030044911A1
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/10/116,949
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-116-949-33

Query Match

Best Local Similarity 1.1%; Score 15.2; DB 14; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.8e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY

335 CTGGTGATGTCACAGTGC 354
1 |||||

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OM nucleic - nucleic search, using sw model

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Sequence: 1 999cagcgagcttgagtgga.....gtgttcagcgagcgcccg 1355

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 310906

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Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	1.2	18	US-09-244-794A-29	Sequence 29, Appl
2	16.4	1.2	18	US-09-007-005-29	Sequence 29, Appl
3	16.4	1.2	18	US-09-247-190-29	Sequence 29, Appl
4	16.4	1.2	18	US-09-244-796-29	Sequence 29, Appl
5	16.4	1.2	18	US-09-238-710-29	Sequence 29, Appl
6	15.8	1.2	20	US-09-136-959A-6	Sequence 6, Appl
7	15.8	1.2	20	US-09-556-031-2	Sequence 2, Appl
8	15.8	1.2	20	US-09-702-246-25	Sequence 25, Appl
9	15.8	1.2	20	US-09-322-624-19	Sequence 19, Appl
10	15.4	1.1	20	US-09-422-978-11451	Sequence 11451, A
11	15.2	1.1	20	US-07-977-284A-89	Sequence 89, Appl
12	15.2	1.1	20	US-08-410-540-8	Sequence 8, Appl
13	15.2	1.1	20	US-08-256-426B-89	Sequence 89, Appl
14	15.2	1.1	20	US-09-661-753-55	Sequence 55, Appl
15	15.2	1.1	20	US-09-470-443-33	Sequence 33, Appl
16	15.2	1.1	20	US-09-470-443-43	Sequence 43, Appl
17	15.2	1.1	20	US-09-659-845A-168	Sequence 168, App
18	15.2	1.1	20	US-09-198-452A-1582	Sequence 1582, App
19	15.2	1.1	20	US-09-198-452A-3952	Sequence 3952, App
20	15.2	1.1	15	US-09-081-646-727	Sequence 727, App
21	14.8	1.1	18	US-08-585-684B-2539	Sequence 2539, App
22	14.8	1.1	18	US-09-038-073-2539	Sequence 2539, App
23	14.8	1.1	19	US-08-630-592-14	Sequence 14, Appl
24	14.8	1.1	19	US-08-714-991-14	Sequence 14, Appl
25	14.8	1.1	19	US-09-033-365A-26	Sequence 26, Appl
26	14.8	1.1	20	US-08-623-891-3	Sequence 3, Appl
27	14.8	1.1	20	US-09-286-904-42	Sequence 42, Appl

28	14.8	1.1	20	US-09-742-703-11	Sequence 11, Appl
29	14.8	1.1	20	US-09-340-861-3	Sequence 3, Appl
30	14.8	1.1	20	US-09-634-262-3	Sequence 3, Appl
31	14.8	1.1	20	US-09-640-101-42	Sequence 42, Appl
32	14.4	1.1	17	US-09-359-921-27	Sequence 27, Appl
33	14.4	1.1	18	US-09-178-115-113	Sequence 113, Appl
34	14.4	1.1	18	US-09-177-776-113	Sequence 113, Appl
35	14.4	1.1	20	US-08-376-362A-8	Sequence 8, Appl
36	14.4	1.1	20	US-08-634-331-3	Sequence 134, App
37	14.4	1.1	20	US-08-450-905B-134	Sequence 134, App
38	14.4	1.1	20	US-07-982-759F-134	Sequence 134, App
39	14.4	1.1	20	US-09-280-805-48	Sequence 48, Appl
40	14.4	1.1	20	US-09-150-460B-2	Sequence 2, Appl
41	14.4	1.1	20	US-09-228-942-7	Sequence 7, Appl
42	14.4	1.1	20	US-09-517-467B-240	Sequence 240, App
43	14.2	1.0	19	US-08-246-489-7	Sequence 7, Appl
44	14.2	1.0	20	US-08-033-081B-18	Sequence 18, Appl
45	14.2	1.0	20	US-08-117-952-417	Sequence 417, App

ALIGNMENTS

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RESULT 1
US-09-244-794A-29
; Sequence 29, Application US/09244794A
; Patent No. 6214553
; GENERAL INFORMATION:
; APPLICANT: Scostak, Jack W.
; APPLICANT: Roberts, Richard W.
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350006
; CURRENT APPLICATION NUMBER: US/09/244,794A
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-244-794A-29
Query Match          1.2%; Score 16.4; DB 3; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy      679 GTGGTATTGGGAGCCAG 696
      |||||||
Db      1 GTGGTATTGGGAGCCAG 18
RESULT 2
US-09-007-005-29
; Sequence 29, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Scostak, Jack W.
; APPLICANT: Roberts, Richard W.
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963

```

EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-007-005-29

Query Match 1.2% Score 16.4; DB 3; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 679 GTGGATTGTGAGCCAG 696
|||||
DB 1 GTGGATTGTGAGCCAG 18

RESULT 3

US-09-247-190-29
Sequence 29, Application US/09247190
Patent No. 6261804
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihne
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350005
CURRENT APPLICATION NUMBER: US/09/247,190
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-21
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-247-190-29

Query Match 1.2% Score 16.4; DB 3; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 679 GTGGATTGTGAGCCAG 696
|||||
DB 1 GTGGATTGTGAGCCAG 18

RESULT 4

US-09-244-796-29
Sequence 29, Application US/09244796
Patent No. 6281344
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihne
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06

EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-244-796-29

Query Match 1.2% Score 16.4; DB 3; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 679 GTGGATTGTGAGCCAG 696
|||||
DB 1 GTGGATTGTGAGCCAG 18

RESULT 5

US-09-238-710-29
Sequence 29, Application US/09238710A
Patent No. 6518018
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihne
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350004
CURRENT APPLICATION NUMBER: US/09/238,710A
CURRENT FILING DATE: 1999-01-28
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-238-710-29

Query Match 1.2% Score 16.4; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 679 GTGGATTGTGAGCCAG 696
|||||
DB 1 GTGGATTGTGAGCCAG 18

RESULT 6

US-09-136-959A-6
Sequence 6, Application US/09136959A
Patent No. 6248522
GENERAL INFORMATION:
APPLICANT: HABERHAUSEN, Gerd
APPLICANT: JOGER, Stephan
APPLICANT: SOBEK, Harald
TITLE OF INVENTION: REDUCTION OF CROSS-CONTAMINATIONS IN NUCLEIC ACID
FILE REFERENCE: 1614-8065
CURRENT APPLICATION NUMBER: US/09/136,959A
CURRENT FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: DE 197 36 062.9
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6

LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-136-959A-6

Query Match 1.2%; Score 15.8; DB 3; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 274 ATCAAGAGAGACAG 292
|||||
DB 1 ATCAATGAGAGAGCTCAG 19

RESULT 7
US-09-556-031-2/c
Sequence 2, Application US/09556031
Patent No. 6350868
GENERAL INFORMATION:
APPLICANT: Weston, Brent W.
APPLICANT: Hiller, Kara B.
TITLE OF INVENTION: Antisense Fucosyltransferase Sequences and Methods of
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: Weston and Hiller
CURRENT APPLICATION NUMBER: US/09/556,031
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/131,068
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:antisense
US-09-556-031-2

Query Match 1.2%; Score 15.8; DB 4; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1322 CTTTGTAGATCTGTGTT 1340
|||||
DB 19 CTTTGTAGATCTTCAGTT 1

RESULT 8
US-09-702-246-25/c
Sequence 25, Application US/09702246
Patent No. 6383809
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOCHESIN-1 EXPRESSION
FILE REFERENCE: RTS-0195
CURRENT APPLICATION NUMBER: US/09/702,246
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 25
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-246-25

Query Match 1.2%; Score 15.8; DB 4; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 521 ACCTCCGAGAGAGCT 539
|||||
DB 20 ACCTCCGAGAGAGCTCCT 2

RESULT 9
US-09-322-624-19
Sequence 19, Application US/09322624
Patent No. 6548734
GENERAL INFORMATION:
APPLICANT: Glimcher, L et al.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MODULATION OF
TITLE OF INVENTION: CARTILAGE GROWTH BY MODULATION OF NTP ACTIVITY
FILE REFERENCE: HUI-035CP
CURRENT APPLICATION NUMBER: US/09/322,624
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: USSN 09/087,139
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 20
TYPE: DNA
ORGANISM: synthetic construct
US-09-322-624-19

Query Match 1.2%; Score 15.8; DB 4; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 934 CTGAGAGAGGTGTGAGC 952
|||||
DB 1 CTGAGAGAGAGCTATGAGC 19

RESULT 10
US-09-422-978-11451/c
Sequence 11451, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSEP.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 11451
LENGTH: 20
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..20
OTHER INFORMATION: downstream amplification primer 99-6707 for SEQ 3586, in compl
US-09-422-978-11451

Query Match 1.1%; Score 15.4; DB 4; Length 20;
Best Local Similarity 94.1%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 225 TCTCAGCTCAGGCAAT 241
|||||
DB 17 TCTCAGCTCAGGCAAT 1

RESULT 11
US-07-977-284A-89/C
Sequence 89, Application US/07977284A
Patent No. 5558988
GENERAL INFORMATION:
APPLICANT: Brockop, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Williams, Charlene J.
APPLICANT: Rivanien, Pertti
APPLICANT: Baldwin, Clinton
APPLICANT: Hopkinson, Ian
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988rls
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,284A
FILING DATE: 13-NOV-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0697
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
ANTI-SENSE: NO
US-07-977-284A-89

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. NO. 2.6e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 282 GGAAGCAGCAGCATGTCTG 301
DB 20 GGAAGCAGCAGCAGCTGACAG 1

RESULT 12
US-08-410-540-8/C
Sequence 8, Application US/08410540
Patent No. 5807678
GENERAL INFORMATION:
APPLICANT: Miller, Walter L.
APPLICANT: Lin, Dong
APPLICANT: Strauss III, Jerome F.
TITLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,540
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nealey, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-238/00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 853 5070
TELEFAX: 415 857 0663
TELEX: 380816CCOLEYPA
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-410-540-8

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. NO. 2.6e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 548 TGCTGGCAGCAGTCACACA 567
DB 20 TGCTGGCAGCAGTCACACA 1

RESULT 13
US-08-256-426B-89/C
Sequence 89, Application US/08256426B
Patent No. 5948611
GENERAL INFORMATION:
APPLICANT: Brockop, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Williams, Charlene J.
APPLICANT: Rivanien, Pertti
APPLICANT: Baldwin, Clinton
APPLICANT: Hopkinson, Ian
TITLE OF INVENTION: Methods of Detecting A Genetic
NUMBER OF SEQUENCES: 293
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611rls
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,426B
FILING DATE: 03-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10964
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,284
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mark Deluca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUD-1082
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
ANTI-SENSE: NO
US-08-256-426B-89

Query Match 1.1%; Score 15.2; DB 2; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.6e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 282 GGAGCAGCAGCATGCTG 301
DB 20 GGAGCAGCAGCATGCTGAC 1

RESULT 14
US-09-661-753-55
Sequence 55, Application US/09661753
Patent No. 6436809
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
FILE REFERENCE: ISPH-0498
CURRENT APPLICATION NUMBER: US/09/661,753
CURRENT FILING DATE: 2000-09-14
EARLIER APPLICATION NUMBER: 60/154,546
EARLIER FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 55
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-55

Query Match 1.1%; Score 15.2; DB 4; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.6e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 621 CAGGACCGAGCTCCAGAGC 640
DB 1 CCGGACCGAGATGACAGAGC 20

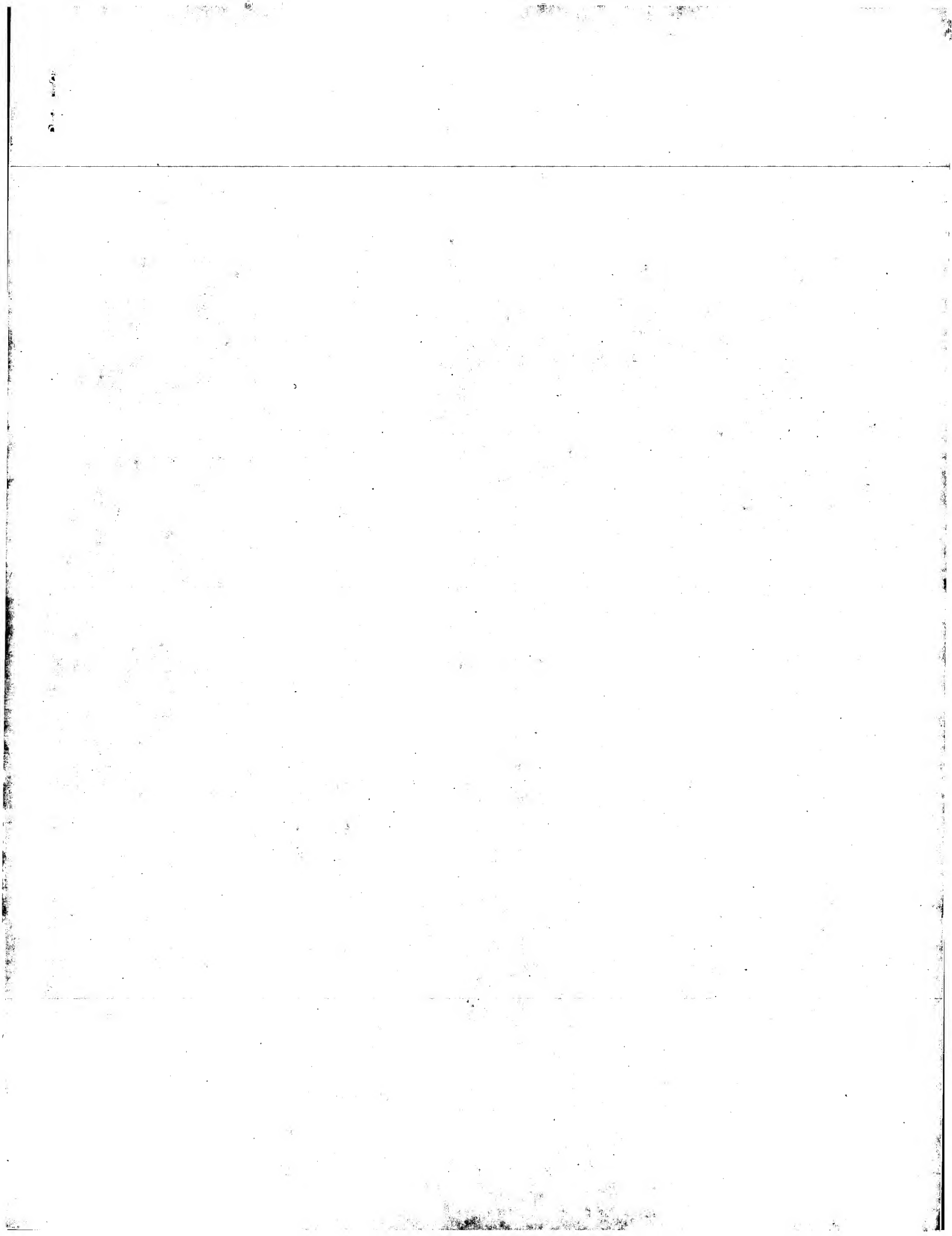
RESULT 15
US-09-470-443-33
Sequence 33, Application US/09470443
Patent No. 6441156
GENERAL INFORMATION:
APPLICANT: Lerman, Michael I.
APPLICANT: Minna, John D.
APPLICANT: Latif, Farida
APPLICANT: Wei, Ming-Hui
APPLICANT: Sekido, Yoshitaka
APPLICANT: Gao, Boning
APPLICANT: Duh, Fuh-Mei

TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
FILE REFERENCE: NIH-05043
CURRENT APPLICATION NUMBER: US/09/470,443
CURRENT FILING DATE: 1999-12-22
EARLIER APPLICATION NUMBER: 60/114,359
EARLIER FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 33
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-470-443-33

Query Match 1.1%; Score 15.2; DB 4; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.6e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 335 CTGGTATAGTCACAGTGC 354
DB 1 CTGGTATAGTCACAGAGC 20

Search completed: September 7, 2003, 20:05:23
Job time: 98.5886 secs



PT comprises determining at least one single nucleotide polymorphism in
PT mitochondrial DNA associated with the disease in the sample from the
XX subject -
XX
XX
PS Example 9; Page 51; 89pp; English.
XX
CC The present invention describes a novel method for determining the risk
CC of or diagnosing Alzheimer's disease using single nucleotide
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC (mtDNA). In addition, the SNPs identified can be used to identify agents
CC suitable for use in treating Alzheimer's disease. Sequences
CC AAC67301-C67610 are PCR primers used to demonstrate the method of the
CC invention.
XX
XX Sequence 20 BP; 4 A; 3 C; 6 G; 7 T; 0 other;
SQ
Query Match 1.5%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 33 CAGCTACGCAAAATCTTAC 52
ID AAV48107 standard; DNA; 18 BP.
AC AAV48107;
XX
XX 27-OCT-1998 (first entry)
DT
XX
XX Beta-globin fusion primer 18.155.
DE
XX
XX In situ transfection; RNA-protein fusion; binding reagent; antibody;
KW industrial catalyst; ss; PCR; primer; amplification.
XX
XX Synthetic.
OS
XX
XX WO9831700-A1.
PN
XX
XX 23-JUL-1998.
PD
XX
XX 14-JAN-1998; 98WO-US00807.
PF
XX
XX 06-NOV-1997; 97US-0064491.
PR
XX
XX 21-JAN-1997; 97US-0035963.
PR
XX
XX (GEHO) GEN HOSPITAL CORP.
PA
XX
XX Liu R, Roberts RW, Scostak JW;
PI
XX
XX WPI: 1998-414032/35.
DR
XX
XX Selection of specific protein by screening protein-RNA fusions
PT generated in vitro or in situ - useful for, e.g. identifying enzymes
PT and antibodies with altered properties, potentially useful as
PT catalysts or for therapy or diagnosis
XX
XX
XX Disclosure: Page 49; 94pp; English.
PS
XX
XX The primers AAV48107 and AAV48108 were used in the synthesis of a
CC beta-globin fusion construct. This was used in the selection of a
CC specific protein or RNA, by in vitro or in situ translation of candidate
CC RNA molecules to produce RNA-protein fusions, then selecting specific RNA
CC protein fusions. The method is used to select proteins (or DNA encoding
CC them) having altered properties, e.g. for identification of new binding
CC reagents, to identify improved human antibodies or new enzymes. These
CC proteins are potentially useful in diagnosis and therapy, or as
CC industrial catalysts. The methods allow many rounds of selection and
CC amplification to be performed, resulting in enrichment of even very rare
CC molecules and allowing isolation of proteins that bind specifically to

CC almost any compound or catalyze almost any reaction.
XX
XX
XX Sequence 18 BP; 3 A; 2 C; 7 G; 6 T; 0 other;
SQ
Query Match 1.2%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 7.7e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 679 GTGTAATTTGGAGCCAG 696
ID AAC67511 standard; DNA; 18 BP.
AC AAC67511;
XX
XX 14-FEB-2001 (first entry)
DT
XX
XX Alzheimer's disease-linked mitochondrial SNP PCR primer #211.
DE
XX
XX Human; mitochondrial genome; single nucleotide polymorphism; SNP;
KW Alzheimer's disease; mtDNA; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200063441-A2.
PN
XX
XX 26-OCT-2000.
PD
XX
XX 19-APR-2000; 2000WO-US10906.
PF
XX
XX 20-APR-1999; 99US-0130447.
PR
XX
XX 22-OCT-1999; 99US-0160901.
PR
XX
XX (MITO-) MITOKOR.
PA
XX
XX Herrnstadt C, Davis RE;
PI
XX
XX WPI: 2000-672748/65.
DR
XX
XX Diagnosing a subject at the risk for or having Alzheimer's disease
PT comprises determining at least one single nucleotide polymorphism in
PT mitochondrial DNA associated with the disease in the sample from the
PT subject -
XX
XX
XX Example 9; Page 51; 89pp; English.
PS
XX
XX The present invention describes a novel method for determining the risk
CC of or diagnosing Alzheimer's disease using single nucleotide
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC (mtDNA). In addition, the SNPs identified can be used to identify agents
CC suitable for use in treating Alzheimer's disease. Sequences
CC AAC67301-C67610 are PCR primers used to demonstrate the method of the
CC invention.
XX
XX
XX Sequence 18 BP; 7 A; 7 C; 3 G; 1 T; 0 other;
SQ
Query Match 1.2%; Score 16.4; DB 21; Length 18;
Best Local Similarity 94.4%; Pred. No. 7.7e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 23 AACCAAAACCCAGCTACG 40
ID AAAA94334 standard; DNA; 18 BP.
AC AAAA94334
XX
XX

AC AAA94334;
XX
XX 11-JAN-2001 (first entry)
DE Human beta-globin mRNA reverse transcription primer 18,155.
XX
XX Human; beta-globin; RNA-protein fusion; protein library;
KM protein isolation; gene cloning; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200047775-A1.
XX
XX 17-AUG-2000.
XX
XX 01-FEB-2000; 2000WO-US02589.
XX
XX 09-FEB-1999; 99US-0247190.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX
XX Szostak JW, Roberts RW, Liu R;
XX
XX WPI; 2000-533022/48.
XX
XX
XX Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions -
XX
XX
XX Disclosure; Page 55; 121pp; English.
XX
XX The present sequence is a primer which was used to generate beta-globin
CC cDNA from mRNA by reverse transcription. The cDNA was used in a method
CC for generating beta-globin RNA-protein fusions. RNA-protein fusions
CC comprise a protein covalently linked to the 3' end of its own mRNA. The
CC fusions are made by synthesis and in vitro or in situ translation of an
CC RNA molecule with a peptide acceptor attached to its 3' end. The
CC RNA-protein fusions are incubated under high salt conditions to produce
CC a protein library. This method is useful for improving or altering
CC existing proteins, as well as for isolating new proteins and nucleic
CC acid or small molecule targets. It may also be used to improve human or
CC humanised single-chain antibodies for the treatment of a number of
CC diseases. The method is useful for the isolation of proteins with
CC specific binding properties, for screening cDNA libraries and cloning
CC new genes on the basis of protein-protein interactions. Unlike prior
CC art, the new method does not rely on maintaining the integrity of an
CC mRNA:ribosome:nascent chain ternary complex, which is very fragile and
CC is therefore of limited use. The method does not rely on topological
CC links between the protein and the nucleic acid so that the information
CC of the protein is retained and can be recovered in readable, nucleic
CC acid form.
XX
XX
XX Sequence 18 BP; 3 A; 2 C; 7 G; 6 T; 0 other;
SQ
Query Match 1.2%; Score 16.4; DB 21; Length 18;
Best Local Similarity 94.4%; Pred. No. 7.7e+05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 679 GTGGTATTGGAGCCAG 696
DB 1 GTGGTATTGGAGCCAG 18
RESULT 5
AAAX22417
ID AAX22417 standard; DNA; 20 BP.
XX
XX AAX22417;
XX
XX 20-MAR-2003 (updated).
DT 19-MAY-1999 (first entry)
XX

DE EP-897990 Seq ID 6.
XX
XX Cross-contamination; amplification; N-lauroylsarcosine; inhibition;
KM reactivation; uracil-N-glycosylase; UNG; false negative; primer; ss.
XX
XX Synthetic.
XX
XX EP897990-A2.
XX
XX 24-FEB-1999.
XX
XX 18-AUG-1998; 98EP-0115491.
XX
XX 20-AUG-1997; 97DE-1036062.
XX
XX (BOEF) BOEHRINGER MANNHEIM GMBH.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
XX Haberhausen G, Jaeger S, Sobek H;
XX
XX WPI; 1999-134649/12.
XX
XX
XX Prevention of cross-contamination in DNA amplification - using
PT nucleic-acid-degrading enzyme and reagent that inhibits reactivation
PT of inactivated enzyme
XX
XX Example 2; Page 8; 17pp; German.
XX
XX This sequence is used to describe a method for reducing
CC cross-contamination during the amplification of nucleic acids in a
CC sample. The method involves (i) treating the sample with an enzyme
CC that degrades nucleic acids from other amplification reactions; (ii)
CC inactivating the enzyme; and (iii) amplifying the nucleic acids in the
CC sample in the presence of a reagent that inhibits reactivation of the
CC enzyme. N-lauroylsarcosine is used to inhibit reactivation of
CC uracil-N-glycosylase (UNG). The new method prevents cross-contamination
CC from amplification products containing artificially introduced dUTP
CC units by using UNG and inhibiting reactivation of the UNG as above
CC (Updated on 20-MAR-2003 to correct PA field.)
XX
XX
XX Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;
SQ
Query Match 1.2%; Score 15.8; DB 20; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 274 ATCAAGAGGAGGAGCAG 292
DB 1 ATCAATGAGGAGGAGCAG 19
RESULT 6
AAC68751/C
ID AAC68751 standard; DNA; 20 BP.
XX
XX AAC68751;
XX
XX 20-FEB-2001 (first entry)
DT
XX
XX Human FUT3 antisense oligonucleotide SEQ ID NO: 2.
DE
XX
XX Human; fucosyltransferase; FUT3; FUT6; cancer; antisense oligonucleotide;
KM PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200064262-A1.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-US10547.
XX

PR 26-APR-1999; 99US-0131068.
XX (UYNC-) UNIV NORTH CAROLINA.
XX Weston BM, Hiller KM.
XX WPI; 2000-687246/67.
DR Novel antisense human fucosyltransferase sequences useful for treating
XX cancer including breast, lung, gastric, renal and uterine cancer
PT
XX
XX
PS Claim 6; Page 32; 53pp; English.
XX
CC The present invention provides antisense oligonucleotides to the human
CC fucosyltransferase coding sequences, particularly FUT3 and FUT6. These
CC antisense sequences can be used in the treatment of cancer, especially
CC colon, pancreatic, ovarian, gastric, breast, lung, hepatocellular,
CC prostate, bladder, renal cell and uterine cancers. In addition, they can
CC also be used in the treatment of animals such as dogs, cats and horses.
XX
SQ Sequence 20 BP; 11 A; 3 C; 3 G; 3 T; 0 other;
Query Match 1.2%; Score 15.8; DB 21; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1322 CTTTGTGATCTTGTCTT 1340
DB 19 CTTTGTGATCTTCACTT 1
RESULT 7
AAZ45870
ID AAZ45870 standard; DNA; 20 BP.
AC AAZ45870;
XX
XX
DT 25-APR-2000 (first entry)
XX
XX
DE PCR primer R1570RAP used to amplify a portion of the RAP3 gene.
XX
XX
KW RAP3; regeneration association protein 3; liver regeneration;
KW liver proliferation; PCR primer; ss.
XX
XX
OS Homo sapiens.
OS
PN WO200003013-A2.
PN
XX
PD 20-JAN-2000.
XX
XX
PE 12-JUL-1999; 99WO-EP04938.
XX
XX
PR 10-JUL-1998; 98EP-0202336.
XX
XX
PA (AMST-) AMSTERDAM MOLECULAR THERAPEUTICS BV.
XX
XX
PI Chamuleau RAFM, Groenink M, Van Der Vliet HN, Leegwater ACJ;
XX WPI; 2000-147615/13.
XX
XX
PT Isolated RAP3 gene, protein and antibody useful for diagnosing liver
PT regeneration and/or cell proliferation -
XX
XX
PS Disclosure; Page 3; 42pp; English.
XX
CC AAZ45864-71 represent PCR primers, derived from the human RAP3 cDNA
CC sequence. The RAP3 (regeneration association protein 3) gene is
CC involved in regeneration processes of the liver. The RAP3 gene was
CC found to be upregulated 6 hours after partial hepatectomy, after
CC which it is downregulated. The PCR primers are useful for detecting
CC nucleotide sequences in a source material. The RAP3 cDNA sequence
CC is useful as a marker of liver proliferation. The RAP3 protein is
CC useful for the diagnosis of liver regeneration and liver cell

CC proliferation. RAP3 antibodies, PCR primers and probes are useful
CC for detecting the occurrence of liver cell proliferation in a patient.
CC The RAP3 protein is also useful for enhancing the growth of
CC regeneration of liver tissue comprising treating the liver tissue
CC such as extracorporeal or intracorporeal.
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;
Query Match 1.2%; Score 15.8; DB 21; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 551 TGGCAGGATGCACACT 569
DB 1 TGGCAGGATGCACACT 19
RESULT 8
AAZ60204
ID AAZ60204 standard; CDNA; 20 BP.
AC AAZ60204;
XX
XX
DT 25-APR-2000 (first entry)
XX
XX
DE PCR primer F1570RAP for RAP3 identification or amplification.
XX
XX
KW RAP3; rat; liver regeneration; hepatic cell proliferation; liver biopsy;
KW liver transplant; bioartificial liver; PCR primer; ss.
XX
XX
OS Rattus sp.
OS
PN EP976824-A1.
PN
XX
PD 02-FEB-2000.
XX
XX
PE 10-JUL-1998; 98EP-0202336.
XX
XX
PR 10-JUL-1998; 98EP-0202336.
XX
XX
PA (AMST-) AMSTERDAM MOLECULAR THERAPEUTICS BV.
XX
XX
PI Chamuleau RAFM, Groenink M, Van der Vliet HN, Leegwater ACJ;
XX WPI; 2000-147615/13.
XX
XX
PT Isolated RAP3 gene, protein and antibody useful for diagnosing liver
PT regeneration and/or cell proliferation -
XX
XX
PS Claim 15; Page 3; 31pp; English.
XX
XX
CC This sequence represents a PCR primer which is based on the rat RAP3
CC gene. The RAP3 gene and rap3 protein are involved in the regeneration
CC processes of the liver, and the RAP3 gene is expressed specifically in
CC the liver. The RAP3 gene is useful for designing PCR primers (such as the
CC present sequence) and probes for detecting nucleotide sequences in a
CC source material and as a marker of liver proliferation. The rap3 protein
CC is useful for the diagnosis of liver regeneration and/or liver cell
CC proliferation. Anti-rap3 antibodies, PCR primers and nucleotide sequences
CC which act as probes are useful for detecting the occurrence of liver cell
CC proliferation in a patient. Single stranded oligonucleotides that are
CC complementary to RAP3 can be used as probes to detect the amount of mRNA
CC transcribed from RAP3 present in a sample such as a liver biopsy, plasma
CC or serum of a tissue or body fluid in comparison to a reference sample.
CC The probes can also be used for screening a liver cDNA or genomic
CC library. The rap3 protein is useful for enhancing the growth or
CC regeneration of liver tissue. The methods of the invention can be used to
CC establish the efficacy of therapeutic agents stimulating liver
CC regeneration and for patients who have undergone liver transplantation
CC and for monitoring patients treated with a bioartificial liver.
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;

Query Match 1.2%; Score 15.8; DB 21; Length 20;
 Best Local Similarity 89.5%; Pred. No. 1.2e+06;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 551 TGGCAGGATGCACACT 569
 1 TGGCAGGATGCACACT 19

RESULT 9

AAZ56049
 ID AAZ56049 standard; DNA; 20 BP.

AC AAZ56049;

DT 23-MAR-2000 (first entry)

DE PCR primer for beta-actin.

XX Nuclear factor of activated T cells; NFATp; bone fracture; osteoporosis;

KW calcineurin interaction region; cartilage cell differentiation;

KW endochondral ossification; chondrosarcoma; rheumatoid arthritis;

KW osteoarthritis; osteosarcoma; fibrous sarcoma; chondroma; enchondroma;

XX PCR primer; beta-actin; ss.

OS Mus sp.

XX WO9961908-A1.

PD 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11941.

XX 28-MAY-1998; 98US-0087139.

XX (HARD) HARVARD COLLEGE.

XX Glimcher LH, Ranger AM;

DR WPI; 2000-086734/07.

XX Modulating growth or differentiation of cartilage cells useful for

XX treating chondrosarcoma, osteochondroma and arthritis in mammals

XX Example 6; Page 57; 90pp; English.

XX PCR primers AAZ56049-256050 are used to amplify beta-actin from wild

XX type and NFATp-/- cartilage cultures. The primers are used in the

XX identification of the role that NFATp plays in cartilage cell growth and

XX differentiation. The modulation of growth or differentiation of

XX cartilage can be carried out through contacting cells deficient in the

XX NFAT family genes, with a test compound. Modulating growth or

XX differentiation of cartilage cells can be achieved by contacting the cells

XX with a modulator of NFAT activity, where the modulator comprises a

XX peptidic compound derived from the calcineurin interacting region of

XX NFATp. The methods of the invention are useful for modulating the growth

XX or differentiation of cartilage cells and endochondral ossification

XX useful for repairing bone defects and fractures in mammals including

XX humans, monkeys, dogs, cats, mice etc. The compound that modulates

XX cartilage cell growth and differentiation is useful for diagnosing

XX disorders such as chondrosarcoma, osteochondroma, chondromyxoid fibroma,

XX chondroma, enchondroma, chondroblastoma, osteoblastoma, fibrous

XX dysplasia, ossifying fibroma, osteosarcoma or osteocartilaginous

XX exostosis, which are associated with a change (elevated, reduced or

XX mutated) in the expression of NFATp in cartilage cell. NFATp inhibitory

XX compounds are useful for treating disorders such as rheumatoid arthritis,

XX osteoarthritis and osteoporosis associated with cartilage degradation.

XX Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 other;

XX Query Match 1.2%; Score 15.8; DB 21; Length 20;

XX Best Local Similarity 89.5%; Pred. No. 1.2e+06;

XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 934 CTGGAGAGAGCTGTGACC 952
 1 CTGGAGAGAGAGCTGTGACC 19

RESULT 10

AAH25407
 ID AAH25407 standard; DNA; 20 BP.

AC AAH25407;

DT 22-AUG-2001 (first entry)

DE Detection probe for a HIV DNA fragment.

XX Magnetic glass particle; nucleic acid purification; probe; ss.

XX Human Immunodeficiency virus.

OS Key Location/Qualifiers

FT modified_base 1 /tag= a

FT /note= "ruthenium3+-(tris-bipyridyl)-derivatisation"

XX WO200137291-A1.

PD 25-MAY-2001.

XX 17-NOV-2000; 2000WO-EP11459.

XX 17-NOV-1999; 99EP-0122853.

XX 12-MAY-2000; 2000EP-0110165.

XX (HOF) ROCHE DIAGNOSTICS GMBH.

XX Weindel K, Riedling M, Geiger A;

DR WPI; 2001-381247/40.

XX Novel composition of magnetic glass particles for purification of DNA

XX or RNA in automated processes

XX Example 7; Page 96; 105pp; English.

XX The specification describes a composition of magnetic glass particles,

XX which contain at least one magnetic object with a mean diameter between

XX 5-500 nm. The composition is useful for the purification of nucleic

XX acids. The composition can be used to process large quantities of

XX nucleic acid samples, because it does not involve the particles being

XX centrifuged or the fluids being drawn through glass fiber filters.

XX The present sequence represents a probe for a HIV DNA fragment. The

XX DNA fragment can be purified using the method of the invention.

XX Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

XX Query Match 1.2%; Score 15.8; DB 22; Length 20;

XX Best Local Similarity 89.5%; Pred. No. 1.2e+06;

XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX OY 274 ATCAAGAGGACGACAG 292
 1 ATCAAGAGGACGACAG 19

RESULT 11

ABST3911/c
 ID ABST3911 standard; DNA; 20 BP.

XX AC ABST3911;

XX DT 06-DEC-2002 (first entry)

DE Human cytohesin-1 coding region antisense oligonucleotide. ISIS#111004.
XX
KW Human; antisense; cytohesin-1; guanine nucleotide exchange protein;
KM ARF; ADP ribosylation factor; inflammation; antiinflammatory; tumour;
KW cytosolic; ss.
XX
OS Homo sapiens.
XX
FN WO200268584-A2.
XX
PD 06-SEP-2002.
XX
PF 30-OCT-2001; 2001WO-US47583.
XX
PR 22-FEB-2001; 2001US-0791243.
XX
PA (ISIS-) ISIS PHARM INC.
XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Bennett CF, Rothlein R, Kishimoto TK, Cowse LT;
XX
DR WPI; 2002-723198/78.
XX
PT New antisense oligonucleotide encoding human cytohesin-1, useful for
PT preventing or treating a disease or condition associated with
PT cytohesin-1 expression e.g. tumor or inflammation
XX
XX Example 15; Page 80; 107pp; English.
XX
PS The invention relates to a new antisense compound, comprising 8-30
CC nucleobases targeted to a nucleic acid molecule encoding human
CC cytohesin-1, specifically hybridises with, and inhibits the expression
CC of human cytohesin-1, a guanine nucleotide exchange protein for ARF
CC (ADP ribosylation factor). The antisense compound may be used in a
CC pharmaceutical composition for inhibiting the expression of
CC cytohesin-1 in human cells or tissues, and in treating a disease or
CC condition associated with cytohesin-1 by administering to the human the
CC antisense compound e.g. tumour or inflammation. The antisense
CC compound is also useful for diagnostics, therapeutics, prophylaxis and
CC as research reagents and kits. The present sequence is an antisense
CC oligonucleotide targeting human cytohesin-1.
XX
SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 other;
Query Match 1.2%; Score 15.8; DB 24; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 521 ACCGCGGAGAGCAGCT 539
DB 20 ACCGCGGAGAGCAGCTCTCT 2
RESULT 12
ABN83653
ID ABN83653 standard; DNA; 20 BP.
XX
AC ABN83653;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human immunodeficiency virus capture probe.
XX
KW Nucleic acid detection; infection; subtilisin; esperase; diagnosis;
KM HIV; probe; ss.
XX
OS Human immunodeficiency virus.
XX
FH Key modified_base 1 Location/Qualifiers
FT /*tag- a
FT /mod_base- OTHER
FT /note- "Ruthenium-tris(bipyridyl) label"

XX
PN EP1201752-A1.
XX
PD 02-MAY-2002.
XX
XX 31-OCT-2000; 2000EP-0123728.
XX
PF 31-OCT-2000; 2000EP-0123728.
XX
PR 31-OCT-2000; 2000EP-0123728.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Schmuck R, Staepels J, Meier T, Wernes U, Russmann E;
XX
DR WPI; 2002-396142/43.
XX
PT Use of Bacillus lentus subtilisin 147 to analyze one or more target
PT non-proteinaceous components from a mixture of non-proteinaceous and
PT proteinaceous components derived from a biological sample useful e.g.
PT diagnostically
XX
PS Example; Page 24; 36pp; English.
XX
CC The present sequence is a human immunodeficiency virus (HIV)
CC capture probe, labeled with ruthenium-tris(bipyridyl) label. The
CC probe was used with HIV PCR primers (see ABN83651-52) in an example
CC from the invention for the amplification and detection of HIV RNA
CC in a plasma sample. The invention provides a method for the
CC analysis of non-proteinaceous components, especially DNA and/or
CC RNA, in a mixture of proteinaceous and non-proteinaceous components
CC in a biological sample. The sample is incubated with protease
CC subtilisin 147 (see ABN76400) of Bacillus lentus variant 147
CC (NCIB 10147), and the target DNA or RNA is then amplified by PCR
CC and determined or detected. In the present example, the
CC ruthenium-tris(bipyridyl)-labeled capture probe provided a
CC sensitive nonisotopic approach to detection based on
CC electrochemiluminescence following specific hybridisation to
CC biotinylated denatured HIV amplicons. The method is useful in
CC environmental, food and medical analysis, e.g. to detect viral
CC infection, and in molecular biological research, and can be
CC performed using a high throughput format.
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;
Query Match 1.2%; Score 15.8; DB 24; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 274 ATCAATGAGAGAGCAGCAG 292
DB 1 ATCAATGAGAGAGCAGCTGCAG 19
RESULT 13
ABG6447/C
ID ABG6447 standard; DNA; 20 BP.
XX
AC ABG6447;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human cytohesin-1 mRNA levels inhibitor #16.
XX
KW Cytohesin-1; CTL; inhibit; cytosolic; antiinflammatory; cytosolic;
KM anti-infective; antisense gene therapy; infection; inflammation; tumour;
KW human; ss; inhibitor.
XX
OS Synthetic.
XX
FH US6383809-B1.
XX
PN 07-MAY-2002.
XX
PD 30-OCT-2000; 2000US-0702246.
PF

XX 30-OCT-2000; 2000US-0702246.
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowsett LM;
XX WPI: 2002-478385/51.
XX
XX New antisense compounds directed against human cytohesin-1, useful for
XX treating and preventing infection, inflammation and tumors
XX
XX Claim 14; Column 41; 40pp; English.
XX
XX The invention relates to a novel antisense compound of 16-30 nucleotides
XX targeted to any of 71 specified regions of the sequence that encodes
XX human cytohesin-1 (CTL), where the compound hybridises and inhibits
XX expression of human CTL. The compound of the invention has
XX antiinflammatory, cytostatic, and anti-infective activity. The
XX antisense compounds may have a use in antisense gene therapy. The
XX antisense compounds are useful for treating or preventing disorders
XX associated with expression of human CTL, e.g. infections, inflammation
XX and tumours, and as research and diagnostic reagents. Sequences
XX AB066432-AB066511 represent chimeric phosphorothioate oligonucleotides,
XX with 2'-MOE wings and a deoxy gap. The claimed sequences inhibit
XX production of cytohesin-1 mRNA.
XX
SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 other;

Query Match 1.2%; Score 15.8; DB 24; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 521 ACCTGCGGAGAGCAGCT 539
|||||
Db 20 ACCTGCGGAGAGCTCT 2

RESULT 14
ABK51604
ID ABK51604 standard; DNA; 20 BP.
XX
AC ABK51604;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human immunodeficiency virus (HIV) protease; probe.
XX
KW Subtilisin 147; medical analysis; environmental analysis;
KW food analysis; diagnostic; virus infection; probe; ss;
KW human immunodeficiency virus; HIV; protease.
XX
OS Human immunodeficiency virus.
XX
PN EPI201753-A1.
XX
PD 02-MAY-2002.
XX
PF 26-OCT-2001; 2001EP-0125322.
XX
PR 31-OCT-2000; 2000EP-0123728.
XX
PR 15-MAR-2001; 2001EP-0106308.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Russmann E, Schmuck R, Meier T, Staepels J, Wehnes U;
XX WPI: 2002-428566/46.
XX
DR Use of Bacillus lentus subtilisin 147 to analyse a target
XX non-proteinaceous component from a mixture of non-proteinaceous and
XX proteinaceous components derived from a biological sample useful e.g.
PT

PT diagnostically to detect viruses
XX
XX Example 2; Page 26; 38pp; English.
XX
XX The invention describes a target non-proteinaceous component is
XX analysed from a mixture of non-proteinaceous and proteinaceous components
XX derived from a biological sample by incubating the mixture with a
XX protease having at least 80 % identity to the known amino acid sequence
XX for subtilisin 147 from Bacillus lentus. The methods are useful for
XX analysis of biological samples e.g. in medical, environmental or food
XX analysis or in molecular biological research. They are especially useful
XX in diagnostics e.g. to detect virus infections. They can be used to
XX enrich a mixture for a target non-proteinaceous component or
XX purify/isolate the component, the component can especially be a nucleic
XX acid, e.g. from a virus/microorganism. The methods can be used to
XX isolate non-proteinaceous components useful as substrates in enzymatic
XX reactions, or (in the case of nucleic acids) for sequencing, as probes
XX etc. They can be used in high throughput formats, enabling analysis of
XX large numbers of samples in a short time. Kits for undertaking the
XX methods, comprising the preferred polypeptide, optionally a material
XX with an affinity to nucleic acids (especially preferred materials as
XX above) and/or optionally lysis, washing and elution buffers are provided.
XX This sequence represents a probe used to detect DNA sequences encoding
XX Human immunodeficiency virus proteases.
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

Query Match 1.2%; Score 15.8; DB 24; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 274 ATCAAAGAGAGAGCAGCAG 292
|||||
Db 1 ATCAATGAGAGAGCTGCAG 19

RESULT 15
ABA04617/C
ID ABA04617 standard; DNA; 20 BP.
XX
XX ABA04617;
XX
DT 21-FEB-2002 (first entry)
XX
DE M02 forward PCR primer.
XX
DE
KW M01; G-coupled protein-receptor; cardiomyopathy; atherosclerosis;
KW cell signal processing; metabolic disorder; diabetes; cancer;
KW neurodegenerative disorder; immune disorder; cardiac disorder;
KW lung disease; autoimmune disease; developmental disorder; antidiabetic;
KW Cystostatic; Neuroprotective; Antiatherosclerotic; Immunosuppressive;
KW Gene therapy; Vaccine; antiinflammatory; PCR primer; ss.
XX
XX Synthetic.
XX
PN WO200181578-A2.
XX
PD 01-NOV-2001.
XX
PF 26-APR-2001; 2001WO-US13578.
XX
PR 26-APR-2000; 2000US-200158P.
PR 28-APR-2000; 2000US-200613P.
PR 28-APR-2000; 2000US-200780P.
PR 01-MAY-2000; 2000US-201006P.
PR 01-MAY-2000; 2000US-201007P.
PR 01-MAY-2000; 2000US-201236P.
PR 01-MAY-2000; 2000US-201238P.
PR 02-MAY-2000; 2000US-201186P.
PR 03-MAY-2000; 2000US-201474P.
PR 03-MAY-2000; 2000US-201508P.
PR 25-JUL-2000; 2000US-220591P.
PR 15-SEP-2000; 2000US-232678P.
PR

PR 22-JAN-2001; 2001US-263217P.
PR 30-JAN-2001; 2001US-265160P.

PA (CURA-) CURAGEN CORP.

PI Vernet CAM, Fernandes ER, Gerlach V, Shinkels RA, Malysankar UM;
PI Boldog FL, Zernusen BD, Splyek KA, Majunder K, Tchernev VT;
PI Padigaru M, Paturajan M, Burgess CE, Gangoli EA, Smithson G;
PI Rastelli L, Macdougall JR, Taupier RJ, Grosse WM, Szekeres ES;
PI Alsbrook JP;

DR WPI: 2002-049278/06.

PT Novel G-protein coupled receptor-related polypeptides and
PT polynucleotides for diagnosing, preventing and treating cardiomyopathy,
PT atherosclerosis, disorders related to cell signal processing and for
PT identifying modulators

PS Example 1, Page 156; 227pp; English.

XX
XX
CC The present invention relates to novel G-coupled protein-receptor related
CC proteins and coding sequences (MOLX, where X is a number from 1 to 10,
CC ABA04589-ABA04603 and AAM47659-AAM47673). MOLX proteins and coding
CC sequences are useful for treating or preventing a MOLX-associated
CC disorder, such as cardiomyopathy, atherosclerosis, disorders related to
CC cell signal processing and metabolic pathway modulation, diabetes and
CC cancer. Additionally, MOLX proteins and coding sequences are useful for
CC preventing and treating a variety of disorders including metabolic
CC disorders, nutritional oedema, chronic and hereditary pancreatitis,
CC obesity, infectious disease, anorexia, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, stroke, immune disorders,
CC haematopoietic disorders and various dyslipidaemias, metabolic syndrome X
CC and wasting disorders associated with chronic diseases and cancers,
CC cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiogenesis
CC and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,
CC multiple sclerosis, lung diseases including asthma, Crohn's disease,
CC scleroderma, autoimmune diseases, developmental disorders and neural tube
CC defects. The present sequence is a PCR primer, which was used to
CC illustrate the invention.

XX
S0 Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 other;

Query Match 1.2%; Score 15.8; DB 24; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 641 TCTGCATCCCCCAGACCT 659
||| ||||| ||||| |||
DB 19 TCTGCATCCACCAAGACAT 1

Search completed: September 7, 2003, 22:34:46
Job time : 367.485 secs